

<110> CuraGen Corporation et al.  
 Alsobrook II, John  
 Eichen, Joseph  
 Lepley, Denise M.  
 Miller, Charles E.  
 Mezes, Peter  
 Hahne, William

**10/578234**  
**1AP20 Rec'd FCT/PTO 03 MAY 2006**

<120> COMPOSITIONS AND METHODS OF USE FOR A FIBROBLAST GROWTH FACTOR

<130> Cura-57 SNP

<140> \*\*\*Enter Current Patent Application ID\*\*\*

<141> 2004-11-3

<150> 10/702,126

<151> 2003-11-4

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<170> CuraSeqList version 0.1

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Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro						
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ggt	ttc	ctg	ggc	ggt	ctg	gag	ggt	ctg	ggt	cag	cag	gtt	ggt	tct	cac	48	
Gly	Phe	Leu	Gly	Gly	Leu	Glu	Gly	Leu	Gly	Gln	Gln	Val	Gly	Ser	His		
1				5					10					15			
ttc	ctg	ctg	ccg	ccg	gct	ggt	gaa	cgt	ccg	cca	ctg	ctg	ggt	gaa	cgt	96	
Phe	Leu	Leu	Pro	Pro	Ala	Gly	Glu	Arg	Pro	Pro	Leu	Leu	Gly	Glu	Arg		
			20					25					30				
cgc	tcc	gca	gct	gaa	cgc	tcc	gct	cgt	ggt	ggc	ccg	ggt	gct	gct	cag	144	
Arg	Ser	Ala	Ala	Glu	Arg	Ser	Ala	Arg	Gly	Gly	Pro	Gly	Ala	Ala	Gln		
		35					40					45					
ctg	gct	cac	ctg	cat	ggt	atc	ctg	cgt	cgc	cgt	cag	ctg	tac	tgc	cgt	192	
Leu	Ala	His	Leu	His	Gly	Ile	Leu	Arg	Arg	Arg	Gln	Leu	Tyr	Cys	Arg		
	50					55					60						
act	ggt	ttc	cac	ctg	cag	atc	ctg	ccg	gat	ggt	tct	gtt	cag	ggt	acc	240	
Thr	Gly	Phe	His	Leu	Gln	Ile	Leu	Pro	Asp	Gly	Ser	Val	Gln	Gly	Thr		
65					70					75				80			
cgt	cag	gac	cac	tct	ctg	ttc	ggt	atc	ctg	gaa	ttc	atc	tct	gtt	gct	288	
Arg	Gln	Asp	His	Ser	Leu	Phe	Gly	Ile	Leu	Glu	Phe	Ile	Ser	Val	Ala		
				85					90					95			

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gtt ggt ctg gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg ggt 336  
 Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly  
 100 105 110

atg aac gac aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct gaa 384  
 Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu  
 115 120 125

tgc atc ttc cgt gaa cag ttt gaa gag aac tgg tac aac acc tac tct 432  
 Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser  
 130 135 140

tcc aac atc tac aaa cat ggt gac acc ggc cgt cgc tac ttc gtt gct 480  
 Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala  
 145 150 155 160

ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt cac 528  
 Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His  
 165 170 175

cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt gtt 576  
 Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val  
 180 185 190

cca gaa ctg tat aaa aac ctg ctg atg tac acc taa 612  
 Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr  
 195 200

<210> 15  
 <211> 203  
 <212> PRT  
 <213> Homo sapiens

<400> 15  
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 1 5 10 15  
 Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg  
 20 25 30  
 Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln  
 35 40 45  
 Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg  
 50 55 60  
 Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr  
 65 70 75 80  
 Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala  
 85 90 95  
 Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly  
 100 105 110  
 Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu  
 115 120 125  
 Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser

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130	135	140	
Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala			
145	150	155	160
Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His			
	165	170	175
Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val			
	180	185	190
Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr			
	195	200	
<210> 16			
<211> 603			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (1)..(600)			
<400> 16			
ggc ggt ctg gag ggt ctg ggt cag cag gtt ggt tct cac ttc ctg ctg			48
Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu			
1	5	10	15
ccg ccg gct ggt gaa cgt ccg cca ctg ctg ggt gaa cgt cgc tcc gca			96
Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala			
	20	25	30
gct gaa cgc tcc gct cgt ggt ggc ccg ggt gct gct cag ctg gct cac			144
Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His			
	35	40	45
ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc cgt act ggt ttc			192
Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe			
	50	55	60
cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt acc cgt cag gac			240
His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp			
	65	70	75
cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt gct gtt ggt ctg			288
His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu			
	85	90	95
gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg ggt atg aac gac			336
Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp			
	100	105	110
aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct gaa tgc atc ttc			384
Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe			
	115	120	125
cgt gaa cag ttt gaa gag aac tgg tac aac acc tac tct tcc aac atc			432
Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile			
	130	135	140

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tac aaa cat ggt gac acc ggc cgt cgc tac ttc gtt gct ctg aac aaa 480  
 Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys  
 145 150 155 160

gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt cac cag aaa ttc 528  
 Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe  
 165 170 175

acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt gtt cca gaa ctg 576  
 Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu  
 180 185 190

tat aaa aac ctg ctg atg tac acc taa 603  
 Tyr Lys Asn Leu Leu Met Tyr Thr  
 195 200

&lt;210&gt; 17

&lt;211&gt; 200

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu  
 1 5 10 15

Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala  
 20 25 30

Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His  
 35 40 45

Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe  
 50 55 60

His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp  
 65 70 75 80

His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu  
 85 90 95

Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp  
 100 105 110

Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe  
 115 120 125

Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile  
 130 135 140

Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys  
 145 150 155 160

Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe  
 165 170 175

Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu  
 180 185 190

Tyr Lys Asn Leu Leu Met Tyr Thr  
 195 200

<210> 18  
 <211> 594  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(591)

<400> 18  
 gag ggt ctg ggt cag cag gtt ggt tct cac ttc ctg ctg ccg ccg gct 48  
 Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala  
 1 5 10 15  
 ggt gaa cgt ccg cca ctg ctg ggt gaa cgt cgc tcc gca gct gaa cgc 96  
 Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg  
 20 25 30  
 tcc gct cgt ggt ggc ccg ggt gct gct cag ctg gct cac ctg cat ggt 144  
 Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly  
 35 40 45  
 atc ctg cgt cgc cgt cag ctg tac tgc cgt act ggt ttc cac ctg cag 192  
 Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln  
 50 55 60  
 atc ctg ccg gat ggt tct gtt cag ggt acc cgt cag gac cac tct ctg 240  
 Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu  
 65 70 75 80  
 ttc ggt atc ctg gaa ttc atc tct gtt gct gtt ggt ctg gtt tct atc 288  
 Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile  
 85 90 95  
 cgt ggt gtt gac tct ggc ctg tac ctg ggt atg aac gac aaa ggc gaa 336  
 Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu  
 100 105 110  
 ctg tac ggt tct gaa aaa ctg acc tct gaa tgc atc ttc cgt gaa cag 384  
 Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln  
 115 120 125  
 ttt gaa gag aac tgg tac aac acc tac tct tcc aac atc tac aaa cat 432  
 Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His  
 130 135 140  
 ggt gac acc ggc cgt cgc tac ttc gtt gct ctg aac aaa gac ggt acc 480  
 Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr  
 145 150 155 160  
 ccg cgt gat ggt gct cgt tct aaa cgt cac cag aaa ttc acc cac ttc 528  
 Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe  
 165 170 175  
 ctg ccg cgc cca gtt gac ccg gag cgt gtt cca gaa ctg tat aaa aac 576  
 Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn  
 180 185 190  
 ctg ctg atg tac acc taa 594

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Leu Leu Met Tyr Thr  
195

&lt;210&gt; 19

&lt;211&gt; 197

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala  
1 5 10 15

Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg  
20 25 30

Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly  
35 40 45

Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln  
50 55 60

Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu  
65 70 75 80

Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile  
85 90 95

Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu  
100 105 110

Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln  
115 120 125

Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His  
130 135 140

Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr  
145 150 155 160

Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe  
165 170 175

Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn  
180 185 190

Leu Leu Met Tyr Thr  
195

&lt;210&gt; 20

&lt;211&gt; 567

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(564)

&lt;400&gt; 20

cac ttc ctg ctg ccg ccg gct ggt gaa cgt ccg cca ctg ctg ggt gaa  
His Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu

48



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1	5	10	15	
cgt cgc tcc gca gct gaa cgc tcc gct cgt ggt ggc ccg ggt gct gct	96			
Arg Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala				
20 25 30				
cag ctg gct cac ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc	144			
Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys				
35 40 45				
cgt act ggt ttc cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt	192			
Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly				
50 55 60				
acc cgt cag gac cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt	240			
Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val				
65 70 75 80				
gct gtt ggt ctg gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg	288			
Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu				
85 90 95				
ggt atg aac gac aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct	336			
Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser				
100 105 110				
gaa tgc atc ttc cgt gaa cag ttt gaa gag aac tgg tac aac acc tac	384			
Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr				
115 120 125				
tct tcc aac atc tac aaa cat ggt gac acc ggc cgt cgc tac ttc gtt	432			
Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val				
130 135 140				
gct ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt	480			
Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg				
145 150 155 160				
cac cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt	528			
His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg				
165 170 175				
ggt cca gaa ctg tat aaa aac ctg ctg atg tac acc taa	567			
Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr				
180 185				
<210> 21				
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<212> PRT				
<213> Homo sapiens				
<400> 21				
His Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu				
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Arg Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala				
20 25 30				
Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys				
35 40 45				

Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly  
 50 55 60

Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val  
 65 70 75 80

Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu  
 85 90 95

Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser  
 100 105 110

Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr  
 115 120 125

Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val  
 130 135 140

Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg  
 145 150 155 160

His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg  
 165 170 175

Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr  
 180 185

&lt;210&gt; 22

&lt;211&gt; 447

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 22

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 ggcagcgtgc agggcaccgc gcaggaccac agcctcttcg gtatcttggga attcatcagt 120  
 gtggcagtg gactggtcag tattagaggt gtggacagtg gtctctatct tggaatgaat 180  
 gacaaaggag aactctatgg atcagagaaa cttacttccg aatgcacatt tagggagcag 240  
 tttgaagaga actggtataa cacctattca tctaacatat ataaacatgg agacactggc 300  
 cgcaggtatt ttgtggcact taacaaagac ggaactccaa gagatggcgc caggtccaag 360  
 aggcacaga aatttacaca tttcttacct agaccagtgg atccagaaaa agttccagaa 420  
 ttgtacaagg acctactgat gtacact 447

&lt;210&gt; 23

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 23

Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln  
 1 5 10 15

Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu  
 20 25 30

Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile  
 35 40 45

Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu  
 50 55 60

Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln  
 65 70 75 80

Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His  
 85 90 95

Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr  
 100 105 110

Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe  
 115 120 125

Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn  
 130 135 140

Leu Leu Met Tyr Thr  
 145

<210> 24

<211> 537

<212> DNA

<213> Homo sapiens

<400> 24

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atggctccct tagccgaagt cgggggcttt ctgggcggcc tggagggctt gggccagccg 60
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accggcttcc acctgcagat cctgcccgcg ggcagcgtgc agggcacccg gcaggaccac 180
agcctcttcg gtatcttgga attcatcagt gtggcagtgg gactggtcag tattagaggt 240
gtggacagtg gtctctatct tggaatgaat gacaaaggag aactctatgg atcagagaaa 300
cttacttccg aatgcattct tagggagcag tttgaagaga actgggtataa cacctattca 360
tctaacatat ataaacatgg agacactggc cgcagggtatt ttgtggcact taacaaagac 420
ggaactccaa gagatggcgc caggtccaag aggcacgaga aatttacaca tttcttacct 480
agaccagtgg atccagaaa agttccagaa ttgtacaaga acctactgat gtacact 537

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